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Fig.1

GTTTCAGGCA GCGCTGCGTC CTGCTGCGCA CGTGGGAAGC CCTGGCCCCG GCCACCCCCG CGATGCCGCG 70
CGCTCCCCGC TGCCGAGCCG TGCGCTCCCT GCTGCGCAGC CACTACCGCG AGGTGCTGCC GCTGGCCACG 140
TTCGTGCGGC GCCTGGGGCC CCAGGGCTGG CGGCTGGTGC AGCGCGGGGA CCCGGCGGCT TTCCGCGCGC 210
TGGTGGCCCA GTGCCTGGTG TGCGTGCCCT GGGACGCACG GCCGCCCCCC GCCGCCCCCT CCTTCCGCCA 280
GGTGTCCTGC CTGAAGGAGC TGGTGGCCCG AGTGCTGCAG AGGCTGTGCG AGCGCGGCGC GAAGAACGTG 350
CTGGCCTTCG GCTTCGCGCT GCTGGACGGG GCCCGCGGGG GCCCCCCCGA GGCCTTCACC ACCAGCGTGC 420
GCAGCTACCT GCCCAACACG GTGACCGACG CACTGCGGGG GAGCGGGGCG TGGGGGCTGC TGCTGCGCCG 490
CGTGGGCGAC GACGTGCTGG TTCACCTGCT GGCACGCTGC GCGCTCTTTG TGCTGGTGGC TCCCAGCTGC 560
GCCTACCAGG TGTGCGGGCC GCCGCTGTAC CAGCTCGGCG CTGCCACTCA GGCCCGGCCC CCGCCACACG 630
CTAGTGGACC CCGAAGGCGT CTGGGATGCG AACGGGCCTG GAACCATAGC GTCAGGGAGG CCGGGGTCCC 700
CCTGGGCCTG CCAGCCCCGG GTGCGAGGAG GCGCGGGGGC AGTGCCAGCC GAAGTCTGCC GTTGCCCAAG 770
AGGCCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACGC CCGTTGGGCA GGGGTCCTGG GCCCACCCGG 840
GCAGGACGCG TGGACCGAGT GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC 910
CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCCAC CCATCCGTGG GCCGCCAGCA CCACGCGGGC 980
CCCCCATCCA CATCGCGGCC ACCACGTCCC TGGGACACGC CTTGTCCCCC GGTGTACGCC GAGACCAAGC 1050
ACTTCCTCTA CTCCTCAGGC GACAAGGAGC AGCTGCGGCC CTCCTTCCTA CTCAGCTCTC TGAGGCCCAG 1120
CCTGACTGGC GCTCGGAGGC TCGTGGAGAC CATCTTTCTG GGTTCCAGGC CCTGGATGCC AGGGACTCCC 1190
CGCAGGTTGC CCCGCCTGCC CCAGCGCTAC TGGCAAATGC GGCCCCTGTT TCTGGAGCTG CTTGGGAACC 1260
ACGCGCAGTG CCCCTACGGG GTGCTCCTCA AGACGCACTG CCCGCTGCGA GCTGCGGTCA CCCCAGCAGC 1330
CGGTGTCTGT GCCCGGGAGA AGCCCCAGGG CTCTGTGGCG GCCCCCGAGG AGGAGGACAC AGACCCCCGT 1400
CGCCTGGTGC AGCTGCTCCG CCAGCACAGC AGCCCCTGGC AGGTGTACGG CTTCGTGCGG GCCTGCCTGC 1470
GCCGGCTGGT GCCCCCAGGC CTCTGGGGCT CCAGGCACAA CGAACGCCGC TTCCTCAGGA ACACCAAGAA 1540
GTTCATCTCC CTGGGGAAGC ATGCCAAGCT CTCGCTGCAG GAGCTGACGT GGAAGATGAG CGTGCGGGAC 1610
TGCGCTTGGC TGCGCAGGAG CCCAGGGGTT GGCTGTGTTC CGGCCGCAGA GCACCGTCTG CGTGAGGAGA 1680
TCCTGGCCAA GTTCCTGCAC TGGCTGATGA GTGTGTACGT CGTCGAGCTG CTCAGGTCTT TCTTTTATGT 1750
CACGGAGACC ACGTTTCAAA AGAACAGGCT CTTTTTCTAC CGGAAGAGTG TCTGGAGCAA GTTGCAAAGC 1820
ATTGGAATCA GACAGCACTT GAAGAGGGTG CAGCTGCGGG AGCTGTCGGA AGCAGAGGTC AGGCAGCATC 1890
GGGAAGCCAG GCCCGCCCTG CTGACGTCCA GACTCCGCTT CATCCCCAAG CCTGACGGGC TGCGGCCGAT 1960
TGTGAACATG GACTACGTCG TGGGAGCCAG AACGTTCCGC AGAGAAAAGA GGGCCGAGCG TCTCACCTCG 2030
AGGGTGAAGG CACTGTTCAG CGTGCTCAAC TACGAGCGGG CGCGGCGCCC CGGCCTCCTG GGCGCCTCTG 2100
TGCTGGGCCT GGACGATATC CACAGGGCCT GGCGCACCTT CGTGCTGCGT GTGCGGGCCC AGGACCCGCC 2170
GCCTGAGCTG TACTTTGTCA AGGTGGATGT GACGGGCGCG TACGACACCA TCCCCCAGGA CAGGCTCACG 2240
GAGGTCATCG CCAGCATCAT CAAACCCCAG AACACGTACT GCGTGCGTCG GTATGCCGTG GTCCAGAAGG 2310
CCGCCCATGG GCACGTCCGC AAGGCCTTCA AGAGCCACGT CTCTACCTTG ACAGACCTCC AGCCGTACAT 2380
GCGACAGTTC GTGGCTCACC TGCAGGAGAC CAGCCCGCTG AGGGATGCCG TCGTCATCGA GCAGAGCTCC 2450
TCCCTGAATG AGGCCAGCAG TGGCCTCTTC GACGTCTTCC TACGCTTCAT GTGCCACCAC GCCGTGCGCA 2520
TCAGGGGCAA GTCCTACGTC CAGTGCCAGG GGATCCCGCA GGGCTCCATC CTCTCCACGC TGCTCTGCAG 2590
CCTGTGCTAC GGCGACATGG AGAACAAGCT GTTTGCGGGG ATTCGGCGGG ACGGGCTGCT CCTGCGTTTG 2660
GTGGATGATT TCTTGTTGGT GACACCTCAC CTCACCCACG CGAAAACCTT CCTCAGGACC CTGGTCCGAG 2730
GTGTCCCTGA GTATGGCTGC GTGGTGAACT TGCGGAAGAC AGTGGTGAAC TTCCCTGTAG AAGACGAGGC 2800
CCTGGGTGGC ACGGCTTTTG TTCAGATGCC GGCCCACGGC CTATTCCCCT GGTGCGGCCT GCTGCTGGAT 2870
ACCCGGACCC TGGAGGTGCA GAGCGACTAC TCCAGCTATG CCCGGACCTC CATCAGAGCC AGTCTCACCT 2940
TCAACCGCGG CTTCAAGGCT GGGAGGAACA TGCGTCGCAA ACTCTTTGGG GTCTTGCGGC TGAAGTGTCA 3010
CAGCCTGTTT CTGGATTTGC AGGTGAACAG CCTCCAGACG GTGTGCACCA ACATCTACAA GATCCTCCTG 3080
CTGCAGGCGT ACAGGTTTCA CGCATGTGTG CTGCAGCTCC CATTTCATCA GCAAGTTTGG AAGAACCCCA 3150
CATTTTTCCT GCGCGTCATC TCTGACACGG CCTCCCTCTG CTACTCCATC CTGAAAGCCA AGAACGCAGG 3220
GATGTCGCTG GGGGCCAAGG GCGCCGCCGG CCCTCTGCCC TCCGAGGCCG TGCAGTGGCT GTGCCACCAA 3290
GCATTCCTGC TCAAGCTGAC TCGACACCGT GTCACCTACG TGCCACTCCT GGGGTCACTC AGGACAGCCC 3360
AGACGCAGCT GAGTCGGAAG CTCCCGGGGA CGACGCTGAC TGCCCTGGAG GCCGCAGCCA ACCCGGCACT 3430
GCCCTCAGAC TTCAAGACCA TCCTGGACTG ATGGCCACCC GCCCACAGCC AGGCCGAGAG CAGACACCAG 3500
CAGCCCTGTC ACGCCGGGCT CTACGTCCCA GGGAGGGAGG GGCGGCCCAC ACCCAGGCCC GCACCGCTGG 3570
GAGTCTGAGG CCTGAGTGAG TGTTTGGCCG AGGCCTGCAT GTCCGGCTGA AGGCTGAGTG TCCGGCTGAG 3640
GCCTGAGCGA GTGTCCAGCC AAGGGCTGAG TGTCCAGCAC ACCTGCCGTC TTCACTTCCC CACAGGCTGG 3710
CGCTCGGCTC CACCCCAGGG CCAGCTTTTC CTCACCAGGA GCCCGGCTTC CACTCCCCAC ATAGGAATAG 3780
TCCATCCCCA GATTCGCCAT TGTTCACCCC TCGCCCTGCC CTCCTTTGCC TTCCACCCCC ACCATCCAGG 3850
TGGAGACCCT GAGAAGGACC CTGGGAGCTC TGGGAATTTG GAGTGACCAA AGGTGTGCCC TGTACACAGG 3920
CGAGGACCCT GCACCTGGAT GGGGGTCCCT GTGGGTCAAA TTGGGGGGAG GTGCTGTGGG AGTAAAATAC 3990
TGAATATATG AGTTTTTCAG TTTTGAAAAA AAAAAAAAAA AAAAAAAAAA AA 4042

Fig. 2

```
MPRAPRCRAV RSLLRSHYRE VLPLATFVRR LGPQGWRLVQ RGDPAAFRAL   50
VAQCLVCVPW DARPPPAAPS FRQVSCLKEL VARVLQRLCE RGAKNVLAFG  100
FALLDGARGG PPEAFTTSVR SYLPNTVTDA LRGSGAWGLL LRRVGDDVLV  150
HLLARCALFV LVAPSCAYQV CGPPLYQLGA ATQARPPPHA SGPRRRLGCE  200
RAWNHSVREA GVPLGLPAPG ARRRGGSASR SLPLPKRPRR GAAPEPERTP  250
VGQGSWAHPG RTRGPSDRGF CVVSPARPAE EATSLEGALS GTRHSHPSVG  300
RQHHAGPPST SRPPRPWDTP CPPVYAETKH FLYSSGDKEQ LRPSFLLSSL  350
RPSLTGARRL VETIFLGSRP WMPGTPRRLP RLPQRYWQMR PLFLELLGNH  400
AQCPYGVLLK THCPLRAAVT PAAGVCAREK PQGSVAAPEE EDTDPRRLVQ  450
LLRQHSSPWQ VYGFVRACLR RLVPPGLWGS RHNERRFLRN TKKFISLGKH  500
AKLSLQELTW KMSVRDCAWL RRSPGVGCVP AAEHRLREEI LAKFLHWLMS  550
VYVVELLRSF FYVTETTFQK NRLFFYRKSV WSKLQSIGIR QHLKRVQLRE  600
LSEAEVRQHR EARPALLTSR LRFIPKPDGL RPIVNMDYVV GARTFRREKR  650
AERLTSRVKA LFSVLNYERA RRPGLLGASV LGLDDIHRAW RTFVLRVRAQ  700
DPPPELYFVK VDVTGAYDTI PQDRLTEVIA SIIKPQNTYC VRRYAVVQKA  750
AHGHVRKAFK SHVSTLTDLQ PYMRQFVAHL QETSPLRDAV VIEQSSSLNE  800
ASSGLFDVFL RFMCHHAVRI RGKSYVQCQG IPQGSILSTL LCSLCYGDME  850
NKLFAGIRRD GLLLRLVDDF LLVTPHLTHA KTFLRTLVRG VPEYGCVVNL  900
RKTVVNFPVE DEALGGTAFV QMPAHGLFPW CGLLLDTRTL EVQSDYSSYA  950
RTSIRASLTF NRGFKAGRNM RRKLFGVLRL KCHSLFLDLQ VNSLQTVCTN 1000
IYKILLLQAY RFHACVLQLP FHQQVWKNPT FFLRVISDTA SLCYSILKAK 1050
NAGMSLGAKG AAGPLPSEAV QWLCHQAFLL KLTRHRVTYV PLLGSLRTAQ 1100
TQLSRKLPGT TLTALEAAAN PALPSDFKTI LD                    1132
```

Fig. 3

09424686 . 112999

Fig. 4

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>129) PHTC.PRO	Seq2(1>150) P123.PRO	Similarity Index	Gap Number	Gap Length	Consensus Length
(2>124)	(1>117)	31.5	4	6	123

```
                     10        20        30        40        50        60        70        80
PHTC.PRO  KFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLR
          K:L:W:..  VV.L:R.FFYVTE     :: ::YRK::W. : .::I .:LK:  L :V E EV :::. . :: .::LR
P123.PRO  KLLRWIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSI-ADLKKETLAEVQEKEV-EEWKKSLGFAPGKLR
                   10        20        30        40        50        60        70

                     90        100       110       120
PHTC.PRO  FIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERA
          :IPK ..:RPI  M.:  . :. ..:::::.:LT:..K L S L  :
P123.PRO  LIPKKTTFRPI--MTF--NKKIVNSDRKTTKLTTNTKLLNSHLMLKTL
           80        90        100       110       120
```

66627F 98912160

Fig. 5

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>150)	Seq2(1>150)	Similarity	Gap	Gap	Consensus
P123.PRO	EST2P.PRO	Index	Number	Length	Length
(2>148)	(1>146)	21.6	4	5	149

```
                  10        20        30        40        50        60        70        80
P123.PRO  LLRWIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKKETLAEVQEKEVEEWKKSLGFAPGKLRLIP
          ::.W:F :L: .:I: FFY TE  .: : .Y: R.:.W: ::.  I.:  K. L.E :    ::   .  .F..:K:R:IP
EST2P.PRO FISWLFRQLIPKIIQTFFYCTEISSTVTIVYF-RHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLSNFNHSKMRIIP
                  10        20        30        40        50        60        70
                  90        100       110       120       130       140       150
P123.PRO  KKT--TFRPIMTFNKKIVNSDRKTTKLTTNTKLLNSHLMLKTLKNRMFKDPFGFAVFNYDDVMKKYEEFVC
          KK:  .FR I .  :   :.: .. K . :. :  :: :L. L:N:.  .:F.  ::: .:: .: .EF
EST2P.PRO KKSNNEFRIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKR-PTSFT-KIYSPTQIADRIKEFKQ
          80        90        100       110       120       130       140
```


09/424686

09/424686

Fig. 6

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>129)	Seq2(1>150)	Similarity	Gap	Gap	Consensus
PHTC.PRO	EST2P.PRO	Index	Number	Length	Length
(3>85)	(1>80)	23.3	3	3	83

```
                  10        20        30        40        50        60        70        80
PHTC.PRO  FLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRF
          F: WL..  : .::::FFY TE.:   .  : ::R...W:KL :  I :.:K   L : ::.  .::. : :.:  S::R:
EST2P.PRO FISWLFRQLIPKIIQTFFYCTEIS-STVTIVYFRHDTWNKLITPFIVEYFKTY-LVE-NNVCRNHNSYTLSNFNHSKMRI
                  10        20        30        40        50        60        70

                  90        100       110       120
PHTC.PRO  IPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERA
          IPK ..    :     GA .   .   E. .: :::   .:L:Y R.
EST2P.PRO IPKKSNNEFRIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRN
           80        90        100       110       120
```

Fig. 7

Alignment Workspace of Untitled, using Clustal method with PAM250 residue weight table

```
           -KFLXWLFXXLVVXLIRXFFYVTEXXXSXXXXXYYRKXXWXKLXXXXIXXXLKXXXLXXVXEXEVRXHXXXXLX-FXXS
                     10        20        30        40        50        60        70        80
PHTC.PRO   AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPA-LLTS
P123.PRO   -KLLRWIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSI-ADLKKETLAEVQEKEV-EEWKKSLG-FAPG
EST2P.PRO  --FISWLFRQLIPKIIQTFFYCTEIS-STVTIVYFRHDTWNKLITPFIVEYFKTYL---VENNVCRNHNSYTLSNFNHS

           LRXIPKKXX--FRPIXXXXXXXXXX---TXXXEXXXXXLTXXXKXLX---XLXXXXXXXFXXX--FSVXNYXDXXKXXX
                     90        100       110       120       130       140       150       160
PHTC.PRO   LRFIPKPDG--LRPIVNMDYVVGAR---TFRREKRAERLTSRVKAL-----------------FSVLNYERA
P123.PRO   LRLIPKKTT--FRPIMTFN----KK---IVNSDRKTTKLTTNTKLLNSHLMLKTLKNRMFKDPFGFAVFNYDDVMKKYE
EST2P.PRO  MRIIPKKSNNEFR-IIAIPCRGADEEEFTIYKENHKNAIQPTQKILE---YLRNKRPTSFTKI--YSPTQIADRIKEFK
```

09 NOV 99

Fig. 8

```
GTGCCTGCAG AGACCCGTCT GGTGCACTCT GATTCTCCAC TTGCCTGTTG CATGTCCTCG TTCCCTTGTT    70
TCTCACCACC TCTTGGGTTG CCATGTGCGT TTCCTGCCGA GTGTGTGTTG ATCCTCTCGT TGCCTCCTGG   140
TCACTGGGCA TTTGCTTTTA TTTCTCTTTG CTTAGTGTTA CCCCCTGATC TTTTTATTGT CGTTGTTTGC   210
TTTTGTTTAT TGAGACAGTC TCACTCTGTC ACCCAGGCTG GAGTGTAATG GCACAATCTC GGCTCACTGC   280
AACCTCTGCC TCCTCGGTTC AAGCAGTTCT CATTCCTCAA CCTCATGAGT AGCTGGGATT ACAGGCGCCC   350
ACCACCACGC CTGGCTAATT TTTGTATTTT TAGTAGAGAT AGGCTTTCAC CATGTTGGCC AGGCTGGTCT   420
CAAACTCCTG ACCTCAAGTG ATCTGCCCGC CTTGGCCTCC CACAGTGCTG GGATTACAGG TGCAAGCCAC   490
CGTGCCCGGC ATACCTTGAT CTTTTAAAAT GAAGTCTGAA ACATTGCTAC CCTTGTCCTG AGCAATAAGA   560
CCCTTAGTGT ATTTTAGCTC TGGCCACCCC CCAGCCTGTG TGCTGTTTTC CCTGCTGACT TAGTTCTATC   630
TCAGGCATCT TGACACCCCC ACAAGCTAAG CATTATTAAT ATTGTTTTCC GTGTTGAGTG TTTCTTTAGC   700
TTTGCCCCCG CCCTGCTTTT CCTCCTTTGT TCCCCGTCTG TCTTCTGTCT CAGGCCCGCC GTCTGGGGTC   770
CCCTTCCTTG TCCTTTGCGT GGTTCTTCTG TCTTGTTATT GCTGGTAAAC CCCAGCTTTA CCTGTGCTGG   840
CCTCCATGGC ATCTAGCGAC GTCCGGGGAC CTCTGCTTAT GATGCACAGA TGAAGATGTG GAGACTCACG   910
AGGAGGGCGG TCATCTTGGC CCGTGAGTGT CTGGAGCACC ACGTGGCCAG CGTTCCTTAG CCAGGGTTGG   980
CTGTGTTCCG GCCGCAGAGC ACCGTCTGCG TGAGGAGATC CTGGCCAAGT TCCTGCACTG GCTGATGAGT  1050
GTGTACGTCG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA CGGAGACCAC GTTTCAAAAG AACAGGCTCT  1120
TTTTCTACCG GAAGAGTGTC TGGAGCAAGT TGC                                          1153
```

Fig. 9

```
CAGAGCCCTG GTCCTCCTGT CTCCATCGTC ACGTGGGCAC ACGTGGCTTT TCGCTCAGGA CGTCGAGTGG    70
ACACGGTGAT CTCTGCCTCT GCTCTCCCTC CTGTCCAGTT TGCATAAACT TACGAGGTTC ACCTTCACGT   140
TTTGATGGAC ACGCGGTTTC CAGGCACCGA GGCCAGAGCA GTGAACAGAG GAGGGTGGGC GCGGCAGTGG   210
AGCCGGGTTG CCGGCAATGG GGAGAAGTGT CTGGAAGCAC AGACGCTCTG GCGAGGGTGC CTGCAGAGAC   280
CCGCCTGGTG CACTCTGATT CTCCACTTGC CTGTTGCATG TCCTCGTTCC CTTGTTTCTC ACCACCTCTT   350
GGGTTGCCAT GTGCGTTTCC TGCCGAGTGT GTGTTGATCC TCTCGTTGCC TCCTGGTCAC TG           412
```

Fig. 10

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GGGGTCCTGG GCCCACCCGG GCAGGACGCG TGGACCGAGT GACCGTGGTT TCTGTGTGGT GTCACCTGCC    70
AGACCCGCCG AAGAAGCCAC CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCCAC CCATCCGTGG   140
GCCGCCAGCA CCACGCGGGC CCCCCATCCA CATCGCGGCC ACCACGTCCC TGGGACACGC CTTGTCCCCC   210
GGTGTACGCC GAGACCAAGC ACTTCCTCTA CTCCTCAGGC GACAAGGAGC AGCTGCGGCC CTCCTTCCTA   280
CTCAGCTCTC TGAGGCCCAG CCTGACTGGC GCTCGGAGGC TCGTGGAGAC CATCTTTCTG GGTTCCAGGC   350
CCTGGATGCC AGGGACTCCC CGCAGGTTGC CCCGCCTGCC CCAGCGCTAC TGGCAAATGC GGCCCCTGTT   420
TCTGGAGCTG CTTGGGAACC ACGCGCAGTG CCCCTACGGG GTGCTCCTCA AGACGCACTG CCCGCTGCGA   490
GCTGCGGTCA CCCCAGCAGC CGGTGTCTGT GCCCGGGAGA AGCCCCAGGG CTCTGTGGCG GCCCCCGAGG   560
AGGAGGACAC AGACCCCCGT CGCCTGGTGC AGCTGCTCCG CCAGCACAGC AGCCCCTGGC AGGTGTACGG   630
CTTCGTGCGG GCCTGCCTGC GCCGGCTGGT GCCCCCAGGC CTCTGGGGCT CCAGGCACAA CGAACGCCGC   700
TTCCTCAGGA ACACCAAGAA GTTCATCTCC CTGGGGAAGC ATGCCAAGCT CTCGCTGCAG GAGCTGACGT   770
GGAAGATGAG CGTGCGGGAC TGCGCTTGGC TGCGCAGGAG CCCAGGTGAG GAGGTGGTGG CCGTCGAGGG   840
CCCAGGCCCC AGAGCTGAAT GCAGTAGGGG CTCAGAAAAG GGGGCAGGCA GAGCCCTGGT CCTCCTGTCT   910
CCATCGTCAC GTGGGCACAC GTGGCTTTTC GCTCAGGACG TCGAGTGGAC ACGGTGATCT CTGCCTCTGC   980
TCTCCCTCCT GTCCAGTTTG CATAAACTTA CG                                           1012
```

Fig. 11

```
GAATTCGCGG CCGCGTCGAC GTTTCAGGCA GCGCTGCGTC CTGCTGCGCA CGTGGGAAGC CCTGGCCCCG 70
GCCACCCCCG CGATGCCGCG CGCTCCCCGC TGCCGAGCCG TGCGCTCCCT GCTGCGCAGC CACTACCGCG 140
AGGTGCTGCC GCTGGCCACG TTCGTGCGGC GCCTGGGGCC CCAGGGCTGG CGGCTGGTGC AGCGCGGGGA 210
CCCGGCGGCT TTCCGCGCGC TGGTGGCCCA GTGCCTGGTG TGCGTGCCCT GGGACGCACG GCCGCCCCCC 280
GCCGCCCCCT CCTTCCGCCA GGTGTCCTGC CTGAAGGAGC TGGTGGCCCG AGTGCTGCAG AGGCTGTGCG 350
AGCGCGGCGC GAAGAACGTG CTGGCCTTCG GCTTCGCGCT GCTGGACGGG GCCCGCGGGG GCCCCCCCGA 420
GGCCTTCACC ACCAGCGTGC GCAGCTACCT GCCCAACACG GTGACCGACG CACTGCGGGG GAGCGGGGCG 490
TGGGGGCTGC TGCTGCGCCG CGTGGGCGAC GACGTGCTGG TTCACCTGCT GGCACGCTGC GCGCTCTTTG 560
TGCTGGTGGC TCCCAGCTGC GCCTACCAGG TGTGCGGGCC GCCGCTGTAC CAGCTCGGCG CTGCCACTCA 630
GGCCCGGCCC CCGCCACACG CTAGTGGACC CCGAAGGCGT CTGGGATGCG AACGGGCCTG GAACCATAGC 700
GTCAGGGAGG CCGGGGTCCC CCTGGGCCTG CCAGCCCCGG GTGCGAGGAG GCGCGGGGGC AGTGCCAGCC 770
GAAGTCTGCC GTTGCCCAAG AGGCCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACGC CCGTTGGGCA 840
GGGGTCCTGG GCCCACCCGG GCAGGACGCG TGGACCGAGT GACCGTGGTT TCTGTGTGGT GTCACCTGCC 910
AGACCCGCCG AAGAAGCCAC CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCCAC CCATCCGTGG 980
GCCGCCAGCA CCACGCGGGC CCCCCATCCA CATCGCGGCC ACCACGTCCC TGGGACACGC CTTGTCCCCC 1050
GGTGTACGCC GAGACCAAGC ACTTCCTCTA CTCCTCAGGC GACAAGGAGC AGCTGCGGCC CTCCTTCCTA 1120
CTCAGCTCTC TGAGGCCCAG CCTGACTGGC GCTCGGAGGC TCGTGGAGAC CATCTTTCTG GGTTCCAGGC 1190
CCTGGATGCC AGGGACTCCC CGCAGGTTGC CCCGCCTGCC CCAGCGCTAC TGGCAAATGC GGCCCCTGTT 1260
TCTGGAGCTG CTTGGGAACC ACGCGCAGTG CCCCTACGGG GTGCTCCTCA AGACGCACTG CCCGCTGCGA 1330
GCTGCGGTCA CCCCAGCAGC CGGTGTCTGT GCCCGGGAGA AGCCCCAGGG CTCTGTGGCG GCCCCCGAGG 1400
AGGAGGACAC AGACCCCCGT CGCCTGGTGC AGCTGCTCCG CCAGCACAGC AGCCCCTGGC AGGTGTACGG 1470
CTTCGTGCGG GCCTGCCTGC GCCGGCTGGT GCCCCCAGGC CTCTGGGGCT CCAGGCACAA CGAACGCCGC 1540
TTCCTCAGGA ACACCAAGAA GTTCATCTCC CTGGGGAAGC ATGCCAAGCT CTCGCTGCAG GAGCTGACGT 1610
GGAAGATGAG CGTGCGGGAC TGCGCTTGGC TGCGCAGGAG CCCAGGTGAG GAGGTGGTGG CCGTCGAGGG 1680
CCCAGGCCCC AGAGCTGAAT GCAGTAGGGG CTCAGAAAAG GGGGCAGGCA GAGCCCTGGT CCTCCTGTCT 1750
CCATCGTCAC GTGGGCACAC GTGGCTTTTC GCTCAGGACG TCGAGTGGAC ACGGTGATCT CTGCCTCTGC 1820
TCTCCCTCCT GTCCAGTTTG CATAAACTTA CGAGGTTCAC CTTCACGTTT TGATGGACAC GCGGTTTCCA 1890
GGCGCCGAGG CCAGAGCAGT GAACAGAGGA GGCTGGGCGC GGCAGTGGAG CCGGGTTGCC GGCAATGGGG 1960
AGAAGTGTCT GGAAGCACAG ACGCTCTGGC GAGGGTGCCT GCAGGGGTTG GCTGTGTTCC GGCCGCAGAG 2030
CACCGTCTGC GTGAGGAGAT CCTGGCCAAG TTCCTGCACT GGCTGATGAG TGTGTACGTC GTCGAGCTGC 2100
TCAGGTCTTT CTTTTATGTC ACGGAGACCA CGTTTCAAAA GAACAGGCTC TTTTTCTACC GGAAGAGTGT 2170
CTGGAGCAAG TTGCAAAGCA TTGGAATCAG ACAGCACTTG AAGAGGGTGC AGCTGCGGGA GCTGTCGGAA 2240
GCAGAGGTCA GGCAGCATCG GGAAGCCAGG CCCGCCCTGC TGACGTCCAG ACTCCGCTTC ATCCCCAAGC 2310
CTGACGGGCT GCGGCCGATT GTGAACATGG ACTACGTCGT GGGAGCCAGA ACGTTCCGCA GAGAAAAGAG 2380
GGTGGCTGTG CTTTGGTTTA ACTTCCTTTT TAAACAGAAG TGCGTTTGAG CCCCACATTT GGTATCAGCT 2450
TAGATGAAGG GCCCGGAGGA GGGGCCACGG GACACAGCCA GGGCCATGGC ACGGCGCCAA CCCATTTGTG 2520
CGCACGGTGA GGTGGCCGAG GTGCCGGTGC CTCCAGAAAA GCAGCGTGGG GGTGTAGGGG GAGCTCCTGG 2590
GGCAGGGACA GGCTCTGAGG ACCACAAGAA GCAGCTGGGC CAGGGCCTGG ATGCAGCACG GCCCGAGCGG 2660
GTGGGGGCCC ACCACGCCAT TCTGGTCAAA GGTGTTGTAG TCGTAATAGC CGGCCCAGGC GCTCTGAACC 2730
TTCAGAGTCT CAAAAGCTGG GACCCTCAGG GCCAAATGGG GCCACACCTT GTCCTGGAAG AAATCATGGT 2800
CCACTTCCAG GTTCGCCGGG TCCGGTTCTT CCTGCTCAGT GGGGCTACGA CCACCTAGGT AGTTGCTACC 2870
TAATCCTTCC CGGCGAAAAT AGGCTCCACT GGTGTCTGCA ACAAGCGGAG TCTCTAGGCC TGGTCCCTGG 2940
GGGCAGTGCC ACACATACAC ATACCTTTTC CTCGGCTCCA CAGGTAGCTT GGTGCCCTGC AGGGTGCCAG 3010
GCGGCCCCTC TCCAACACCA GCCAGTGCTG CGATTTGCGC AGACCAGGCT CCGGCTGCGT TGATCACAAT 3080
GGCGCATTCC ACAGGCTGGT ACTCCAGGCT GCGGTCCATC TTCACATGGA CTTCATGGAT CCTTTTCAAG 3150
ACCACCGCTT TGTCATCTGT GGTCAACATG CGTTGAGATG AAGAGACAAA ACGTGTCACC TCTCCCTGGC 3220
AGAAAAGGAC TCCCAAGGAC TGGACCTTTC GCCGAAGCCC CTGGAGCAGA CACCAGGGGT CAAACCAACC 3290
TTCGTCCTCC ATCCCATAAG ACGCCAAAGC CACTCCCTCT GTGTTTATCC AGGGAAACTT GTTCCGAAGC 3360
TGATCAGGAG ACATCAGAGA AACTTTGGCT CCCTCCTGCC TCTGCACTTT CACGTTGCTC TCCATGGCTG 3430
CAGCATCCTT TTCTGAAGCC AGCAAGAGGT AGCCCGAGGG GTTGAACCGG AGGTCCAGGG GAGGAGCATC 3500
GACTACGGCC AGGTACTCAT TGATGTTCCG TAGAAAGCTG GCTGAAAAGA GGGAGAGCTG GATGTTCTCA 3570
GGCAATGAGA ACTGCTGACA AATCCCACCT ACTGAGAGCC CAGTGGAGGC CTGTGAATAC GTGTGGTCCC 3640
GTTCCACCAC TAGCACTCGA ATAGCACCTC GTCTGCTCTC CAGCTTCTTC AGCCAATAGG CCACAGACAA 3710
GCCAAGCACC CCACCTCCCA CGATCACCAC ATCCGAGTGC TCGGGAGGCA GGTGGCTGGT GTCTTGCAGT 3780
AGATCACAGG ACCTTCCAGG CAGGATCGAC TTGATCTTCT TCTTAATCTC AGACACCTTT CCATCCCAGT 3850
CCAGAGAAAA GCCTCCTCTG CGCGTGCCTG GCCTCCGGGT CAAGAGGCCC CGGCCCATGC CGTGCGGCAG 3920
AACCCTCCGA ATCATAGCCC CTCTGAGCCC GGGTCGACGC GGCCGCGAAT TC                 3972
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Substitute Sheet (Rule 26)

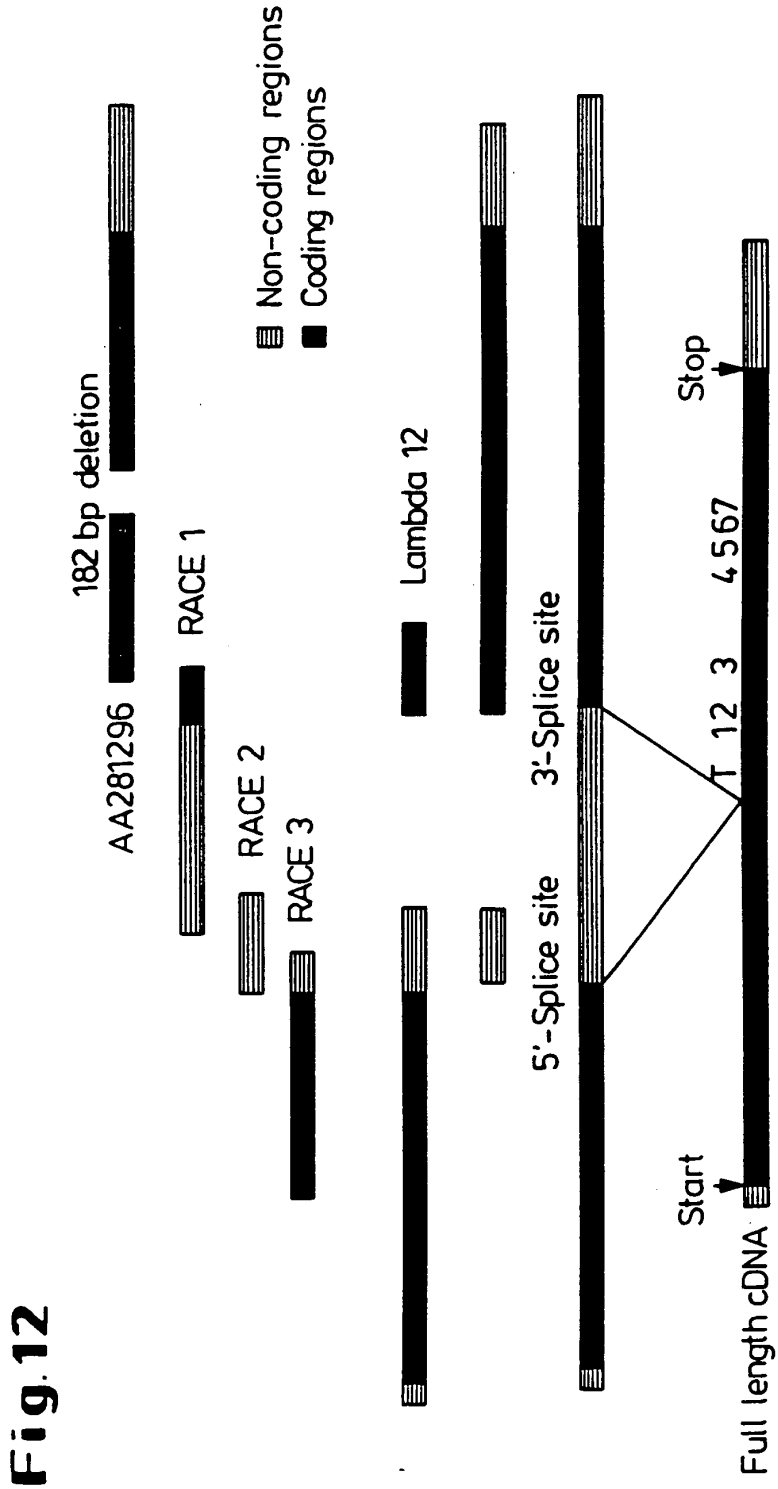

Fig.12

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Fig. 13

Telomerase motif

	553–565
hTC	VVELLRSFFYVTE
Euplotes	VVSLIRCFFYVTE

	RT1 (619–626)	RT2 (630–641)	RT3 (704–720)
RT consens.	p-hh-h-K	hR-h-------K	h--hDh---Y--h
hTC	SRLRFIPK	LRPIVNMDYVVG	PELYFVKVDVTGAYDTI
Euplotes	GKLRLIPK	FRPIMTFNKKIV	PELYFMKFDVKSCYDSI

	RT4 (827–839)	RT5 (863–872)	RT6 (895–902)	RT7 (913–918)
RT consens.	h---hPQG---SP	h--YhDDhhh	Gh-h---K	hLG--h
hTC	QCQGIPQGSILST	LLRLVDDFLL	GCVVNLRK	ALGGTA
Euplotes	QTKGIPQGLCVSS	LMRLTDDYLL	GFKFNMKK	KFAKYG

Fig. 14

CCGGAAGAGT GTCTGGAGCA AGTTGCAAAG CATTGGAATC AGACAGCACT TGAAGAGGGT GCAGCTGCGG 1853
GAGCTGTCGG AAGCAGAGGT CAGGCAGCAT CGGGAAGCCA GGCCCGCCCT GCTGACGTCC AGACTCCGCT 1923
TCATCCCCAA GCCTGACGGG CTGCGGCCGA TTGTGAACAT GGACTACGTC GTGGGAGCCA GAACGTTCCG 1993
CAGAGAAAAG AGGGCCGAGC GTCTCACCTC GAGGGTGAAG GCACTGTTCA GCGTGCTCAA CTACGAGCGG 2063
GCGCGGCGCC CCGGCCTCCT GGGCGCCTCT GTGCTGGGCC TGGACGATAT CCACAGGGCC TGGCGCACCT 2133
TCGTGCTGCG TGTGCGGGCC CAGGACCCGC CGCCTGAGCT GTACTTTGTC AAGGTGGATG TGACGGGCGC 2203
GTACGACACC ATCCCCCAGG ACAGGCTCAC GGAGGTCATC GCCAGCATCA TCAAACCCCA GAACACGTAC 2273
TGCGTGCGTC GGTATGCCGT GGTCCAGAAG GCCGCCCATG GGCACGTCCG CAAGGCCTTC AAGAGCCACG 2343
TCTCTACCTT GACAGACCTC CAGCCGTACA TGCGACAGTT CGTGGCTCAC CTGCAGGAGA CCAGCCCGCT 2413
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CTACGCTTCA TGTGCCACCA CGCCGTGCGC ATCAGGGGCA AGTCCTACGT CCAGTGCCAG GGGATCCCGC 2553
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CCTATTCCCC TGGTGCGGCC TGCTGCTGGA TACCCGGACC CTGGAGGTGC AGAGCGACTA CTCCAGCTAT 2903
GCCCGGACCT CCATCAGAGC CAGTCTCACC TTCAACCGCG GCTTCAAGGC TGGGAGGAAC ATGCGTCGCA 2973
AACTCTTTGG GGTCTTGCGG CTGAAGTGTC ACAGCCTGTT TCTGGATTTG CAGGTGAACA GCCTCCAGAC 3043
GGTGTGCACC AACATCTACA AGATCCTCCT GCTGCAGGCG TACAGGTTTC ACGCATGCGT GCTGCAGCTC 3113
CCATTTCATC AGCAAGTTTG GAAGAACCCC ACATTTTTCC TGCGCGTCAT CTCTGACACG GCCTCCCTCT 3183
GCTACTCCAT CCTGAAAGCC AAGAACGCAG GTATGTGCAG GTGCCTGGCC TCAGTGGCAG CAGTGCCTGC 3253
CTGCTGGTGT TAGTGTGTCA GGAGACTGAG TGAATCTGGG CTTAGGAAGT TCTTACCCCT TTTCGCATCA 3323
GGAAGTGGTT TAACCCAACC ACTGTCAGGC TCGTCTGCCC GCCCTCTCGT GGGGTGAGCA GAGCACCTGA 3393
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GCCTGGTCTC TCCTGTTTGC CCCATGGTGG GATTTGGGGG GCCTGGCCTC TCCTGTTTGC CCTGTGGTGG 3533
GATTGGGCTG TCTCCCGTCC ATGGCACTTA GGGCCCTTGT GCAAACCCAG GCCAAGGGCT TAGGAGGAGG 3603
CCAGGCCCAG GCTACCCCAC CCCTCTCAGG AGCAGAGGCC GCGTATCACC ACGACAGAGC CCCGCGCCGT 3673
CCTCTGCTTC CCAGTCACCG TCCTCTGCCC CTGGACACTT TGTCCAGCAT CAGGGAGGTT TCTGATCCGT 3743
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SUBSTITUTE SHEET (RULE 26)

Fig.15

Fig. A

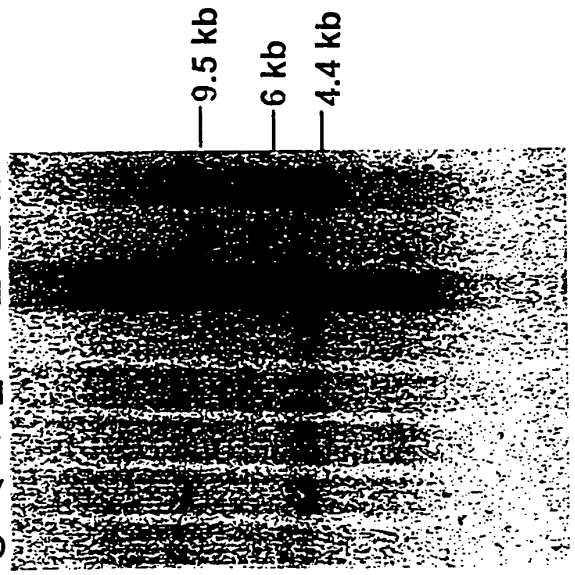
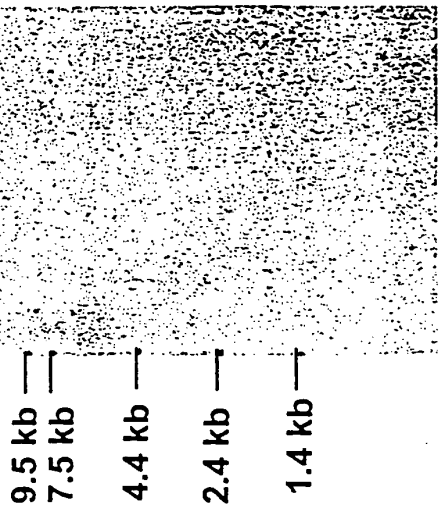


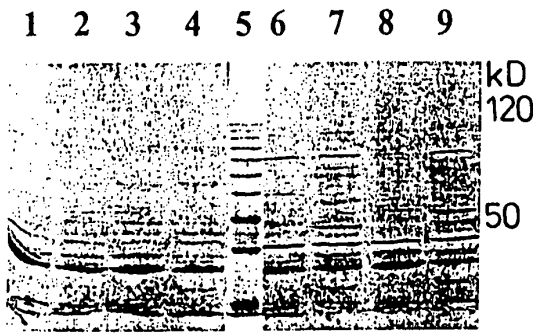
Fig. B



SUBSTITUTE SHEET (RULE 26)

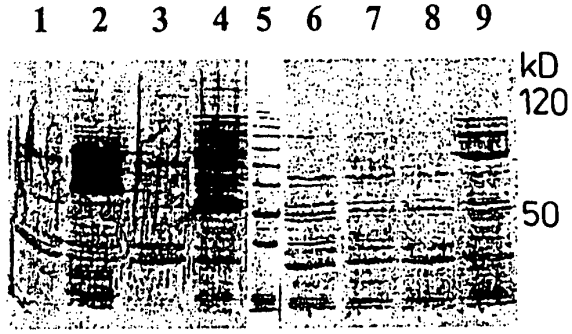
Fig. 16

Fig. A



pMAL EST	pMAL-EST	pMAL AI	pMal AI	M	pMAL-EST	pMAL-EST	pMAL AI	pMAL AI
-	+	-	+		-	+	-	+
anti-B pre-immun					anti-C pre-immun			

Fig. B



pMAL-EST	pMAL-EST	PMAL AI	pMAL AI	M	pMAL-EST	pMAL-EST	pMAL AI	pMAL AI
-	+	-	+		-	+	-	+
anti-B 1° immun.					anti-C 1° immun.			

Fig. 17

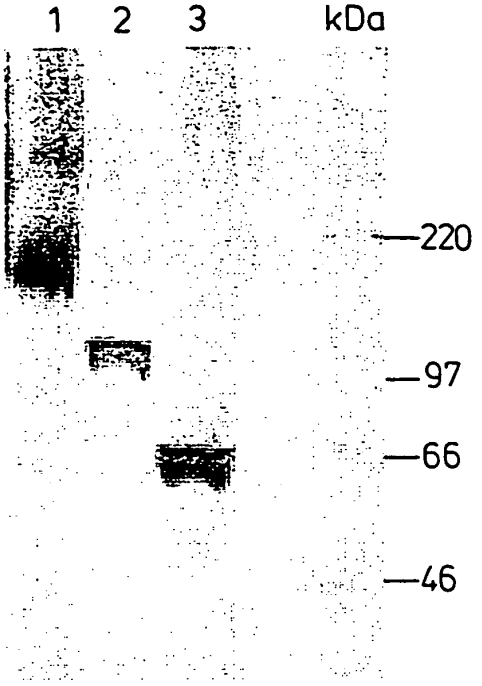


Fig. 19

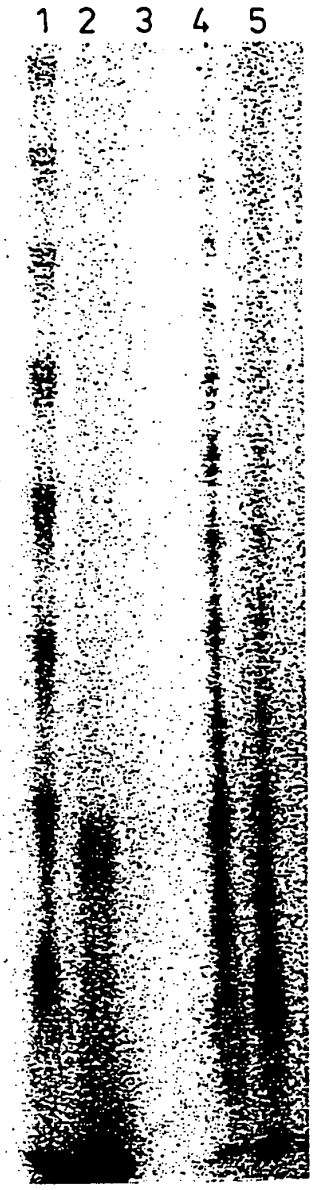
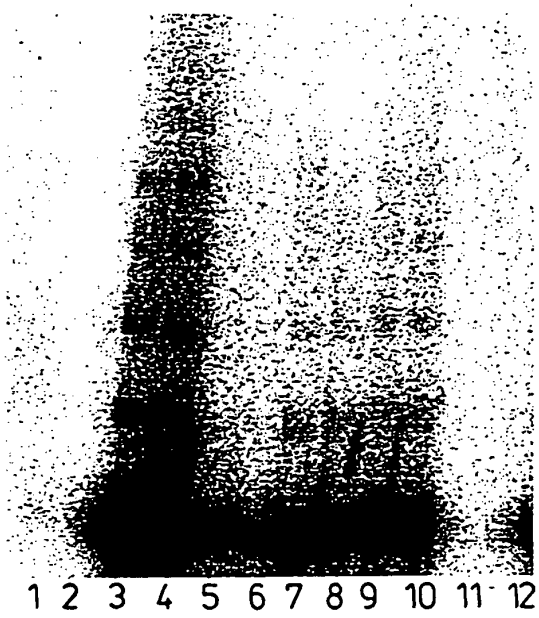


Fig. 18



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